

SECOND SUBSTITUTE SEQUENCE LISTING

<110> Thompson, M. Craig
Long, Fan
Wobbe, C. Richard

<120> A NOVEL FUNGAL MULTISUBUNIT PROTEIN
COMPLEX CRITICAL FOR EXPRESSION OF FUNGAL PROTEINS

<130> 0342/1D516US2

<140> US 09/601,965

<141> 2000-10-20

<150> PCT/US99/02940

<151> 1999-02-08

<150> 60/074,100

<151> 1998-02-09

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<170> FastSEQ for Windows Version 3.0

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<213> C. albicans

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CS
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His	Leu	Glu	Lys	Glu	Gln	Ile	Lys	Arg	Asn	Ile	Lys	Tyr	Tyr	Phe	Pro
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Asp	His	Tyr	Ser	Lys	Asp	Leu	Val	Leu	Ser	Thr	Thr	Asp	Trp	Asp	Asp
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Asp	Ala	Ile	Ile	Asn	Ala	Gly	Asp	Asn	Glu	Tyr	Ser	Ile	Val	Lys	Pro
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His	Arg	Pro	Val	Phe	Asn	Val	Arg	Pro	Gly	Thr	Leu	Val	Ser	Phe	Ser
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Gly Ala Gly Ser His Gln Lys Phe Tyr Leu Arg Gly Ile Asn Phe Asn				
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Phe Ala Val Gly Asn Thr Phe Pro Val Glu Val Pro Ala Pro His Ser				
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Arg Lys Val Thr Asn Ile Ser Lys Asn Arg Leu Lys Met Val Val Phe				
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Arg Val Met Asn Ser Leu Gly Val Pro Arg Ile Ser Val Lys Asp Val				
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Lys Glu Phe Met Glu Tyr Gln Arg Gln Gly Glu Asp Gln Gly Tyr Trp				
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Lys Val Arg Gly Leu Asn Asp Val Ile Pro Gly Glu Glu Glu Ile Arg				
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Lys Glu Val Glu Lys Glu Lys Glu Gln Glu Arg Glu Glu Glu Lys Gly				
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Lys Asp Lys Glu Lys Asp Lys Asp Lys Glu Lys Asp Lys Thr Glu Lys				
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Glu Lys Ser Lys Lys Ser Lys Glu Gln Asp Thr Glu Ile Asp Val Glu				
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Glu Glu Leu Ala Pro Trp Asn Leu Ser Arg Asn Phe Val Ile Ala Asn				
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Gln Thr Lys Thr Met Leu Gln Leu Asn Gly Glu Gly Asp Pro Thr Gly				
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Ile Gly Leu Gly Phe Ser Met Leu Arg Ala Thr Gln Lys Asn Pro Phe				
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	900		905	910
Ala Ala His Asn Gln Lys Leu Tyr Glu Gln Glu Ile Lys Arg Ile Trp				
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Tyr Ser Gln Arg Ser Ser Leu Val Asp His Gly Glu Gly Thr Glu Ser				
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Ile Val His Arg Lys Val Glu Phe Ile His Asp Pro Arg Leu Ile Arg				
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Ala Tyr Val Lys Arg Lys Lys Gln Ile Glu Asp Glu Leu Leu Lys Asn				
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Ala Asp Val Asp Glu Ile Leu Pro Thr Asn Asp Lys Glu Leu Asn Lys				
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Ala Ala Ala Ala Gly Ala Thr Ile Ile Asp Ala Asn Thr Val Met Leu				
1090		1095		1100

Pro Asp Gly Ser Tyr Val Ile Gly Gly Lys Gly Ile Gly Lys Gly Lys
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 Val Leu Gly Ile Asp Ser Asn Ser Leu Asn Met Gln Leu Pro Glu Ile
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 225 230 235 240
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 Val Gln Gln Asp Asp Lys Arg Leu Phe Asn Ser Arg Thr Ile Ser Tyr
 260 265 270
 Val Ala Pro Ile Tyr Gln Gly Lys Asn Asn Leu Leu Gln Ser Asn Ser
 275 280 285
 Ser Ala Ser Arg Arg Gly Leu Ile His Val Ser Ile Asp Glu Leu Phe
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 Pro Ile Lys Glu Gln Gln Lys Lys Arg Lys Ile Ile His Asp Glu Lys
 305 310 315 320
 Thr Ile Ser Glu Asp Leu Leu Ile Ala Thr Asp Asp Trp Asp Gln Glu
 325 330 335
 Lys Ile Ile Asn Gln Gly Thr Ser Ser Thr Ala Thr Leu Ala Asp Ser
 340 345 350
 Ser Met Thr Pro Asn Leu Lys Phe Ser Gly Gly Tyr Lys Leu Lys Ser
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Arg	Leu	Lys	Asp	Asp	Glu	Lys	Leu	Leu	Asp	Asn	Glu	Ala	Val	Lys	Ser	740	745	750
Leu	Ile	Thr	Pro	Glu	Gln	Ile	Ser	Gln	Val	Glu	Ser	Met	Ser	Gln	Gly	755	760	765
Leu	Gln	Phe	Gln	Glu	Asp	Asn	Glu	Ala	Tyr	Asn	Phe	Asp	Ser	Lys	Leu	770	775	780
Lys	Ser	Leu	Glu	Glu	Asn	Leu	Leu	Pro	Trp	Asn	Ile	Thr	Lys	Asn	Phe	785	790	795
Ile	Asn	Ser	Thr	Gln	Met	Arg	Ala	Met	Ile	Gln	Ile	His	Gly	Val	Gly	805	810	815
Asp	Pro	Thr	Gly	Cys	Gly	Glu	Gly	Phe	Ser	Phe	Leu	Lys	Thr	Ser	Met	820	825	830
Lys	Gly	Gly	Phe	Val	Lys	Ser	Gly	Ser	Pro	Ser	Ser	Asn	Asn	Asn	Ser	835	840	845
Ser	Asn	Lys	Lys	Gly	Thr	Asn	Thr	His	Ser	Tyr	Asn	Val	Ala	Gln	Gln			

850		855		860
Gln Lys Ala Tyr Asp Glu	Glu Ile Ala Lys Thr	Trp Tyr Thr His Thr		
865	870	875		880
Lys Ser Leu Ser Ile Ser	Asn Pro Phe Glu	Met Thr Asn Pro Asp		
	885	890		895
Glu Ile Asn Gln Thr	Asn Lys His Val Lys	Thr Asp Arg Asp Asp Lys		
	900	905		910
Lys Ile Leu Lys Ile Val	Arg Lys Lys Arg Asp	Glu Asn Gly Ile Ile		
	915	920		925
Gln Arg Gln Thr Ile Phe	Ile Arg Asp Pro Arg	Val Ile Gln Gly Tyr		
	930	935		940
Ile Lys Ile Lys Glu Gln	Asp Lys Glu Asp Val	Asn Lys Leu Leu Glu		
945	950	955		960
Glu Asp Thr Ser Lys Ile	Asn Asn Leu Glu Glu	Leu Glu Lys Gln Lys		
	965	970		975
Lys Leu Leu Gln Leu Glu	Leu Ala Asn Leu Glu	Lys Ser Gln Gln Arg		
	980	985		990
Arg Ala Ala Arg Gln	Asn Ser Lys Arg Asn	Gly Gly Ala Thr Arg Thr		
	995	1000		1005
Glu Asn Ser Val Asp	Asn Gly Ser Asp Leu	Ala Gly Val Thr Asp Gly		
	1010	1015		1020
Lys Ala Ala Arg Asn	Lys Gly Lys Asn Thr	Thr Arg Arg Cys Ala Thr		
1025	1030	1035		1040
Cys Gly Gln Ile Gly	His Ile Arg Thr Asn	Lys Ser Cys Pro Met Tyr		
	1045	1050		1055
Ser Ser Lys Asp Asn	Pro Ala Ser Pro Lys			
	1060	1065		

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 <211> 979
 <212> PRT
 <213> S. pombe

<400> 4
Met Ser Phe Asp Gly Leu Ile Val Glu Asn Glu Asn Thr Lys Ser Gly
1 5 10 15
Tyr Asn Asp Gly Asn Asp Leu Thr Asp Leu Phe Lys Gln Asn Gly Thr
20 25 30
Asp Met Ser Val Ile Asn Ser Leu Leu Gly Asp Thr Asn Asn Pro Gly
35 40 45
Met Asn Glu Ser Pro Lys Ile Leu Asp Ser Ser Phe Glu Asn Ser Asn
50 55 60
Pro Gln Asp Gly Pro Asn Tyr Glu Asp Phe Asp Phe Met Gly Ser Ile
65 70 75 80
His Lys Glu Phe Gly Asn Asn Ile Asn Glu Met Asp Asp Met Glu Asp
85 90 95
Val Ser Asp Asp Asn Leu Pro Glu Glu Glu Gln Ala Val Asn Tyr Thr
100 105 110
Gly Asp Lys Asp Asp Glu Asp Phe Gly Lys Leu Leu Ala Lys Glu Met
115 120 125
Gly Glu Glu Ala Ala Gly Gln Val Leu Ser Gly Val Gly Phe Ser Ile
130 135 140
Pro Ser Gly Leu Val Pro Ser Glu Pro Ser Lys Thr Val Ser Ser
145 150 155 160
Thr Thr Glu Glu Leu Gln Asn Glu Ala Gln Ile Arg Glu Ser Ile Val
165 170 175
Lys Thr Phe Phe Pro Thr Phe Glu Arg Gly Val Leu Leu Asn Phe Ser
180 185 190
Glu Leu Phe Lys Pro Lys Pro Val Lys Leu Ala Pro Pro Lys Lys Lys
195 200 205
Thr Pro Lys Val Cys Val Pro Gly Arg Leu Thr Leu Glu Val Asp Thr

210	215	220
Asp Tyr Ala Ile Ile Phe	Asn Ser Lys Lys Ser	Leu Pro Leu Lys Arg
225	230	235
Asn Val Val Ser Pro Ile	Ser Thr His Thr Lys	Lys Arg Arg Arg Thr
245	250	255
Ala Asn Thr Ser Gln Arg	Asn Asp Gly Leu Asp	Leu Asn Thr Val Phe
260	265	270
Thr Thr Asn Asp Trp Glu	Lys Asn Ile Ile Tyr	Asp Glu Ser Asp Val
275	280	285
Asn Lys Thr Asn Gln Ser	Ser Phe Phe Ile Asp	Lys Ser Leu Val Asp
290	295	300
Ile Asp Phe Ala Phe Asp	Glu Asn Ile Phe Asp	Gly Asp Thr Gly Thr
305	310	315
Ser Lys Val Val Leu Asn	Leu Asn Asp Pro Lys	Leu Leu Leu Gln Pro
325	330	335
Gln Leu Pro Lys Lys Glu	Asp Ser Gln Arg Ser	Phe Ala Asp Thr His
340	345	350
Gln Arg Asn Ser Leu Ala	Trp Lys Phe Asn Ile	Ser Asn Asp Pro Ala
355	360	365
Tyr Glu Met Leu Lys Gln	Asn His Gln Ser Lys	Val Arg Asn Thr Leu
370	375	380
Ser Gln Leu Ala Ile Glu	His Ala Ala Phe Ala	Glu Lys Leu Thr Phe
385	390	395
Pro Tyr Tyr Lys Thr Arg	Leu Ser Lys Arg Ala	Val Arg Ser Tyr His
405	410	415
Arg Pro Thr Met Ser Phe	Lys Pro Asn Ala Ala	Ile Val Phe Ser Pro
420	425	430
Leu Ile Val Arg Lys Arg	Ser Lys Asp Lys His	Lys Ser Glu Arg Glu
435	440	445
Leu Ile Pro Thr Thr Lys	Glu Ile Thr Met Gly	Asp Thr Thr His Ala
450	455	460
Ile Leu Val Glu Phe Ser	Glu Glu His Pro Ala	Val Leu Ser Asn Ala
465	470	475
Gly Met Ala Ser Arg Ile	Val Asn Tyr Tyr Arg	Lys Lys Asn Glu Gln
485	490	495
Asp Glu Ser Arg Pro Lys	Leu Glu Val Gly Glu	Ser His Val Leu Asp
500	505	510
Val Gln Asp Arg Ser Pro	Phe Trp Asn Phe Gly	Ser Val Glu Pro Gly
515	520	525
Glu Ile Thr Pro Thr Leu	Tyr Asn Lys Met Ile	Arg Ala Pro Leu Phe
530	535	540
Lys His Glu Val Pro Pro	Thr Asp Phe Ile Leu	Ile Arg Asn Ser Ser
545	550	555
Ser Tyr Gly Ser Lys Tyr	Tyr Leu Lys Asn Ile	Asn His Met Phe Val
565	570	575
Ser Gly Gln Thr Phe Pro	Val Thr Asp Val Pro	Gly Pro His Ser Arg
580	585	590
Lys Val Thr Thr Ala Ser	Lys Asn Arg Leu Lys	Met Leu Val Phe Arg
595	600	605
Leu Ile Arg Arg Ser Pro	Asn Gly Gly Leu Phe	Ile Arg Gln Leu Ser
610	615	620
Lys His Phe Ser Asp Gln	Asn Glu Met Gln Ile	Arg Gln Arg Leu Lys
625	630	635
Glu Phe Met Glu Tyr Lys	Lys Lys Gly Asp Gly	Pro Gly Tyr Trp Lys
645	650	655
Leu Lys Ser Asn Glu Val	Val Pro Asp Glu Ala	Gly Thr Arg Ser Met
660	665	670
Val Ser Pro Glu Thr Val	Cys Leu Leu Glu Ser	Met Gln Val Gly Val
675	680	685
Arg Gln Leu Glu Asp Ala	Gly Tyr Gly Lys Thr	Met Asp Glu Ile Asn
690	695	700

Asp Asp Glu Asp Glu Glu Gln Pro Ala Glu Gln Leu Leu Ala Pro Trp
 705 710 715 720
 Ile Thr Thr Arg Asn Phe Ile Asn Ala Thr Gln Gly Lys Ala Met Leu
 725 730 735
 Thr Leu Phe Gly Glu Gly Asp Pro Thr Gly Ile Gly Glu Gly Tyr Ser
 740 745 750
 Phe Ile Arg Thr Ser Met Lys Gly Gly Phe Lys Pro Ala Gly Glu Thr
 755 760 765
 Ala Asp Asp Lys Pro Glu Pro Gln Thr Lys Asn Ala His Ala Tyr Asn
 770 775 780
 Val Ala Lys Gln Gln Arg Ala Tyr Glu Glu Glu Ile Asn Arg Ile Trp
 785 790 795 800
 Asn Ala Gln Lys Arg Gly Leu Ser Ile Asn Asn Leu Glu Glu Leu Ala
 805 810 815
 Lys Lys Tyr Gly Ile Asn Ser Ile His Asp Asp Tyr Val Glu Ser Asn
 820 825 830
 Glu Glu Thr Thr Arg Glu Glu Thr Pro Ser Ser Asp Lys Val Leu Arg
 835 840 845
 Ile Val Arg Leu Tyr Arg Asp Lys Asn Gly Asn Leu Glu Arg Lys Gln
 850 855 860
 Glu Thr Ile His Asp Pro Ile Val Ile His Ala Tyr Leu Lys Lys Arg
 865 870 875 880
 Arg Glu Ile Asp Glu Gln Ser Thr Ala Leu Asp Ala Val Val Pro Thr
 885 890 895
 Gly Asp Glu Ala Ile Asp Arg Arg Asn Arg Arg Arg Leu Glu Gln Glu
 900 905 910
 Leu Ala Lys Ser Gln Lys Asn Trp Glu Arg Arg Arg Ala Arg His Ala
 915 920 925
 Ala Lys Glu Gly Ile Asn Leu Asn Gly Glu Gly Arg Lys Pro Thr Thr
 930 935 940
 Arg Lys Cys Ser Asn Cys Gly Gln Val Gly His Met Lys Thr Asn Lys
 945 950 955 960
 Ile Cys Pro Leu Phe Gly Arg Pro Glu Gly Gly Leu Ala Thr Met Leu
 965 970 975
 Asp Lys Asn

<210> 5
 <211> 2066
 <212> PRT
 <213> Drosophila

<400> 5
 Met Glu Ser Asp Asn Ser Asp Asp Glu Gly Ser Ile Gly Asn Gly Leu
 1 5 10 15
 Asp Leu Thr Gly Ile Leu Phe Gly Asn Ile Asp Ser Glu Gly Arg Leu
 20 25 30
 Leu Gln Asp Asp Asp Gly Glu Gly Arg Gly Gly Thr Gly Phe Asp Ala
 35 40 45
 Glu Leu Arg Glu Asn Ile Gly Ser Leu Ser Lys Leu Gly Leu Asp Ser
 50 55 60
 Met Leu Leu Glu Val Ile Asp Leu Lys Glu Ala Glu Pro Pro Ser Asp
 65 70 75 80
 Asp Glu Glu Glu Glu Asp Ala Arg Pro Ser Ala Val Ser Ala Ser Gly
 85 90 95
 Gly Met Ser Ala Phe Asp Ala Leu Lys Ala Gly Val Lys Arg Glu Glu
 100 105 110
 Arg Glu Asp Gly Ala Val Lys Ala Gln Asp Asp Ala Ile Asp Tyr Ser
 115 120 125
 Asp Ile Thr Glu Leu Ser Glu Asp Cys Pro Arg Thr Pro Pro Glu Glu
 130 135 140

Thr	Ser	Thr	Tyr	Asp	Asp	Leu	Glu	Asp	Ala	Ile	Pro	Ala	Ser	Lys	Val
145				150					155						160
Glu	Ala	Lys	Leu	Thr	Lys	Asp	Asp	Lys	Glu	Leu	Met	Pro	Pro	Pro	Ser
			165						170						175
Ala	Pro	Met	Arg	Ser	Gly	Ser	Gly	Gly	Gly	Ile	Glu	Glu	Pro	Ala	Lys
			180						185					190	
Ser	Asn	Asp	Ala	Ser	Ser	Pro	Ser	Asp	Asp	Ser	Lys	Ser	Thr	Asp	Ser
	195					200						205			
Lys	Asp	Ala	Asp	Arg	Lys	Leu	Asp	Thr	Pro	Leu	Ala	Asp	Ile	Leu	Pro
	210					215					220				
Ser	Lys	Tyr	Gln	Asn	Val	Asp	Val	Arg	Glu	Leu	Phe	Pro	Asp	Phe	Arg
225					230					235					240
Pro	Gln	Lys	Val	Leu	Arg	Phe	Ser	Arg	Leu	Phe	Gly	Pro	Gly	Lys	Pro
			245						250					255	
Thr	Ser	Leu	Pro	Gln	Ile	Trp	Arg	His	Val	Arg	Lys	Arg	Arg	Arg	Lys
		260						265					270		
Arg	Asn	Gln	Ser	Arg	Asp	Gln	Lys	Thr	Thr	Asn	Thr	Gly	Gly	Ser	Asp
	275						280					285			
Ser	Pro	Ser	Asp	Thr	Glu	Glu	Pro	Arg	Lys	Arg	Gly	Phe	Ser	Leu	His
	290					295					300				
Tyr	Ala	Ala	Glu	Pro	Thr	Pro	Ala	Glu	Cys	Met	Ser	Asp	Asp	Glu	Asp
305					310					315					320
Lys	Leu	Leu	Gly	Asp	Phe	Asn	Ser	Glu	Asp	Val	Arg	Pro	Glu	Gly	Pro
			325						330					335	
Asp	Asn	Gly	Glu	Asn	Ser	Asp	Gln	Lys	Pro	Lys	Val	Ala	Asp	Trp	Arg
		340						345					350		
Phe	Gly	Pro	Ala	Gln	Ile	Trp	Tyr	Asp	Ile	Leu	Glu	Val	Pro	Asp	Ser
	355						360					365			
Gly	Glu	Gly	Phe	Asn	Tyr	Gly	Phe	Lys	Thr	Lys	Ala	Ala	Ser	Thr	Ser
	370					375					380				
Ser	Gln	Gln	Gln	Leu	Lys	Asp	Glu	Arg	Arg	Val	Lys	Ser	Pro	Glu	Asp
385					390					395					400
Asp	Val	Glu	Asp	Pro	Ser	Ile	Ala	Asp	Asp	Ala	Phe	Leu	Met	Val	Ser
			405						410					415	
Gln	Leu	His	Trp	Glu	Asp	Asp	Val	Val	Trp	Asp	Gly	Asn	Asp	Ile	Lys
		420						425					430		
Ala	Lys	Val	Leu	Gln	Lys	Leu	Asn	Ser	Lys	Thr	Asn	Ala	Ala	Gly	Trp
	435						440					445			
Leu	Pro	Ser	Ser	Gly	Ser	Arg	Thr	Ala	Gly	Ala	Phe	Ser	Gln	Pro	Gly
	450					455					460				
Lys	Pro	Ser	Met	Pro	Val	Gly	Ser	Gly	Ser	Ser	Lys	Gln	Gly	Ser	Gly
465					470					475					480
Ala	Ser	Ser	Lys	Lys	Ala	Gln	Gln	Asn	Ala	Gln	Ala	Lys	Pro	Ala	Glu
			485						490					495	
Ala	Pro	Asp	Asp	Thr	Trp	Tyr	Ser	Leu	Phe	Pro	Val	Glu	Asn	Glu	Glu
		500						505					510		
Leu	Ile	Tyr	Tyr	Lys	Trp	Glu	Asp	Glu	Val	Ile	Trp	Asp	Ala	Gln	Gln
	515						520					525			
Val	Ser	Lys	Val	Pro	Lys	Pro	Lys	Val	Leu	Thr	Leu	Asp	Pro	Asn	Asp
	530					535					540				
Glu	Asn	Ile	Ile	Leu	Gly	Ile	Pro	Asp	Asp	Ile	Asp	Pro	Ser	Lys	Ile
545					550					555					560
Asn	Lys	Ser	Thr	Gly	Pro	Pro	Pro	Lys	Ile	Lys	Ile	Pro	His	Pro	His
			565						570					575	
Val	Lys	Lys	Ser	Lys	Ile	Leu	Leu	Gly	Lys	Ala	Gly	Val	Ile	Asn	Val
		580						585					590		
Leu	Ala	Glu	Asp	Thr	Pro	Pro	Pro	Pro	Pro	Lys	Ser	Pro	Asp	Arg	Asp
	595						600					605			
Pro	Phe	Asn	Ile	Ser	Asn	Asp	Thr	Tyr	Tyr	Thr	Pro	Lys	Thr	Glu	Pro
	610					615					620				
Thr	Leu	Arg	Leu	Lys	Val	Gly	Gly	Asn	Leu	Ile	Gln	His	Ser	Thr	Pro

625					630					635				640
Val	Val	Glu	Leu	Arg	Ala	Pro	Phe	Val	Pro	Thr	His	Met	Gly	Pro Met
				645					650					655
Asn	Val	Arg	Ala	Phe	His	Arg	Pro	Pro	Leu	Lys	Lys	Tyr	Ser	His Gly
			660					665						670
Pro	Met	Ala	Gln	Ser	Ile	Pro	His	Pro	Val	Phe	Pro	Leu	Leu	Lys Thr
		675					680					685		
Ile	Ala	Lys	Lys	Ala	Lys	Gln	Arg	Glu	Val	Glu	Arg	Ile	Ala	Ser Gly
	690					695				700				
Gly	Gly	Asp	Val	Phe	Phe	Met	Arg	Asn	Pro	Glu	Asp	Leu	Ser	Gly Arg
705					710					715				720
Asp	Gly	Asp	Ile	Val	Leu	Ala	Glu	Phe	Cys	Glu	Glu	His	Pro	Pro Leu
				725					730					735
Ile	Asn	Gln	Val	Gly	Met	Cys	Ser	Lys	Ile	Lys	Asn	Tyr	Tyr	Lys Arg
			740					745					750	
Lys	Ala	Glu	Lys	Asp	Ser	Gly	Pro	Gln	Asp	Tyr	Val	Tyr	Gly	Glu Val
	755						760					765		
Ala	Phe	Ala	His	Thr	Ser	Pro	Phe	Leu	Gly	Ile	Leu	His	Pro	Gly Gln
	770					775					780			
Cys	Ile	Gln	Ala	Ile	Glu	Asn	Asn	Met	Tyr	Arg	Ala	Pro	Ile	Tyr Pro
785					790					795				800
His	Lys	Met	Ala	His	Asn	Asp	Phe	Leu	Val	Ile	Arg	Thr	Arg	Asn Asn
			805						810					815
Tyr	Trp	Ile	Arg	Ser	Val	Asn	Ser	Ile	Tyr	Thr	Val	Gly	Gln	Glu Cys
		820						825					830	
Pro	Leu	Tyr	Glu	Val	Pro	Gly	Pro	Asn	Ser	Lys	Arg	Ala	Asn	Asn Phe
	835					840						845		
Thr	Arg	Asp	Phe	Leu	Gln	Val	Phe	Ile	Tyr	Arg	Leu	Phe	Trp	Lys Ser
	850					855					860			
Arg	Asp	Asn	Pro	Arg	Arg	Ile	Arg	Met	Asp	Asp	Ile	Lys	Gln	Ala Phe
865					870				875					880
Pro	Ala	His	Ser	Glu	Ser	Ser	Ile	Arg	Lys	Arg	Leu	Lys	Gln	Cys Ala
			885					890					895	
Asp	Phe	Lys	Arg	Thr	Gly	Met	Asp	Ser	Asn	Trp	Trp	Val	Ile	Lys Pro
		900					905					910		
Glu	Phe	Arg	Leu	Pro	Ser	Glu	Glu	Glu	Ile	Arg	Ala	Met	Val	Ser Pro
	915						920					925		
Glu	Gln	Cys	Cys	Ala	Tyr	Phe	Ser	Met	Ile	Ala	Ala	Glu	Gln	Arg Leu
	930					935				940				
Lys	Asp	Ala	Gly	Tyr	Gly	Glu	Lys	Phe	Leu	Phe	Ala	Pro	Gln	Glu Asp
945					950				955					960
Asp	Asp	Glu	Glu	Ala	Gln	Leu	Lys	Leu	Asp	Asp	Glu	Val	Lys	Val Ala
			965					970					975	
Pro	Trp	Asn	Thr	Arg	Ala	Tyr	Ile	Gln	Ala	Met	Arg	Gly	Lys	Cys
		980					985					990		
Leu	Leu	Gln	Leu	Ser	Gly	Pro	Ala	Asp	Pro	Thr	Gly	Cys	Gly	Glu Gly
	995					1000						1005		
Phe	Ser	Tyr	Val	Arg	Val	Pro	Asn	Lys	Pro	Thr	Gln	Thr	Lys	Glu Glu
	1010					1015					1020			
Gln	Glu	Ser	Gln	Pro	Lys	Arg	Ser	Val	Thr	Gly	Thr	Asp	Ala	Asp Leu
1025					1030				1035					1040
Arg	Arg	Leu	Pro	Leu	Gln	Arg	Ala	Lys	Glu	Leu	Leu	Arg	Gln	Phe Lys
			1045						1050					1055
Val	Pro	Glu	Glu	Ile	Lys	Lys	Leu	Ser	Arg	Trp	Glu	Val	Ile	Asp
		1060					1065					1070		
Val	Val	Arg	Thr	Leu	Ser	Thr	Glu	Lys	Ala	Lys	Ala	Gly	Glu	Glu Gly
	1075					1080					1085			
Met	Asp	Lys	Phe	Ser	Arg	Gly	Asn	Arg	Phe	Ser	Ile	Ala	Glu	His Gln
	1090					1095				1100				
Glu	Arg	Tyr	Lys	Glu	Glu	Cys	Gln	Arg	Ile	Phe	Asp	Leu	Gln	Asn Arg
1105					1110				1115					1120

Val Leu Ala Ser Ser Glu Val Leu Ser Thr Asp Glu Ala Glu Ser Ser
 1125 1130 1135
 Ala Ser Glu Glu Ser Asp Leu Glu Glu Leu Gly Lys Asn Leu Glu Asn
 1140 1145 1150
 Met Leu Ser Asn Lys Lys Thr Ser Thr Gln Leu Ser Arg Glu Arg Glu
 1155 1160 1165
 Glu Leu Glu Arg Gln Glu Leu Leu Arg Gln Leu Asp Glu Glu His Gly
 1170 1175 1180
 Gly Pro Ser Gly Ser Gly Gly Ala Lys Gly Ala Lys Gly Lys Asp Asp
 1185 1190 1195 1200
 Pro Gly Gln Gln Met Leu Ala Thr Asn Asn Gln Gly Arg Ile Leu Arg
 1205 1210 1215
 Ile Thr Arg Thr Phe Arg Gly Asn Asp Gly Lys Glu Tyr Thr Arg Val
 1220 1225 1230
 Glu Thr Val Arg Arg Gln Pro Val Ile Asp Ala Tyr Ile Lys Ile Arg
 1235 1240 1245
 Thr Thr Lys Asp Glu Gln Phe Ile Lys Gln Phe Ala Thr Leu Asp Glu
 1250 1255 1260
 Gln Gln Lys Glu Glu Met Lys Arg Glu Lys Arg Arg Ile Gln Glu Gln
 1265 1270 1275 1280
 Leu Arg Arg Ile Lys Arg Asn Gln Glu Arg Glu Arg Leu Ala Gln Leu
 1285 1290 1295
 Ala Gln Asn Gln Lys Leu Gln Pro Gly Gly Met Pro Thr Ser Leu Gly
 1300 1305 1310
 Asp Pro Lys Ser Ser Gly Gly His Ser His Lys Glu Arg Asp Ser Gly
 1315 1320 1325
 Tyr Lys Glu Val Ser Pro Ser Arg Lys Lys Phe Lys Leu Lys Pro Asp
 1330 1335 1340
 Leu Lys Leu Lys Cys Gly Ala Cys Gly Gln Val Gly His Met Arg Thr
 1345 1350 1355 1360
 Asn Lys Ala Cys Pro Leu Tyr Ser Gly Met Gln Ser Ser Leu Ser Gln
 1365 1370 1375
 Ser Asn Pro Ser Leu Ala Asp Asp Phe Asp Glu Gln Ser Glu Lys Glu
 1380 1385 1390
 Met Thr Met Asp Asp Asp Asp Leu Val Asn Val Asp Gly Thr Lys Val
 1395 1400 1405
 Thr Leu Ser Ser Lys Ile Leu Lys Arg His Gly Gly Asp Asp Gly Lys
 1410 1415 1420
 Arg Arg Ser Gly Ser Ser Ser Gly Phe Thr Leu Lys Val Pro Arg Asp
 1425 1430 1435 1440
 Ala Met Gly Lys Lys Lys Arg Arg Val Gly Gly Asp Leu His Cys Asp
 1445 1450 1455
 Tyr Leu Gln Arg His Asn Lys Thr Ala Asn Arg Arg Arg Thr Asp Pro
 1460 1465 1470
 Val Val Val Leu Ser Ser Ile Leu Glu Ile Ile His Asn Glu Leu Arg
 1475 1480 1485
 Ser Met Pro Asp Val Ser Pro Phe Leu Phe Pro Val Ser Ala Lys Lys
 1490 1495 1500
 Val Pro Asp Tyr Tyr Arg Val Val Thr Lys Pro Met Asp Leu Gln Thr
 1505 1510 1515 1520
 Met Arg Glu Tyr Ile Arg Gln Arg Arg Tyr Thr Ser Arg Glu Met Phe
 1525 1530 1535
 Leu Glu Asp Leu Lys Gln Ile Val Asp Asn Ser Leu Ile Tyr Asn Gly
 1540 1545 1550
 Pro Gln Ser Ala Tyr Thr Leu Ala Ala Gln Arg Met Phe Ser Ser Cys
 1555 1560 1565
 Phe Glu Leu Leu Ala Glu Arg Glu Asp Lys Leu Met Arg Leu Glu Lys
 1570 1575 1580
 Ala Ile Asn Pro Leu Leu Asp Asp Asp Asp Gln Val Ala Leu Ser Phe
 1585 1590 1595 1600
 Ile Phe Asp Lys Leu His Ser Gln Ile Lys Gln Leu Pro Glu Ser Trp

C1
 Conf.

<211> 1872
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Gly Pro Gly Cys Asp Leu Leu Leu Arg Thr Ala Ala Thr Ile Thr
 1 5 10 15
 Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
 20 25 30
 Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
 35 40 45
 Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
 50 55 60
 His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
 65 70 75 80
 Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
 85 90 95
 Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
 100 105 110
 Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
 115 120 125
 Gly Ser Leu Gln Pro Leu Cys His Ser Asp Tyr Asp Glu Asp Asp Tyr
 130 135 140
 Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
 145 150 155 160
 Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
 165 170 175
 Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met
 180 185 190
 Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
 195 200 205
 Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
 210 215 220
 Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
 225 230 235 240
 Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
 245 250 255
 Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
 260 265 270
 Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
 275 280 285
 Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
 290 295 300
 Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
 305 310 315 320
 Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
 325 330 335
 Arg Val Ala Glu Trp Arg Tyr Gly Pro Ala Arg Leu Trp Tyr Asp Met
 340 345 350
 Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
 355 360 365
 Arg Lys Thr Glu His Glu Pro Val Ile Lys Ser Arg Met Ile Glu Glu
 370 375 380
 Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu
 385 390 395 400
 Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile Ile Trp
 405 410 415
 Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg Ala Ser
 420 425 430
 Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met Ala Tyr
 435 440 445

Asn	Val	Gln	Gln	Gly	Phe	Ala	Ala	Thr	Leu	Asp	Asp	Asp	Lys	Pro	Trp
450						455				460					
Tyr	Ser	Ile	Phe	Pro	Ile	Asp	Asn	Glu	Asp	Leu	Val	Tyr	Gly	Arg	Trp
465					470					475					480
Glu	Asp	Asn	Ile	Ile	Trp	Asp	Ala	Gln	Ala	Met	Pro	Arg	Leu	Leu	Glu
			485					490						495	
Pro	Pro	Val	Leu	Thr	Leu	Asp	Pro	Asn	Asp	Glu	Asn	Leu	Ile	Leu	Glu
		500						505					510		
Ile	Pro	Asp	Glu	Lys	Glu	Glu	Ala	Thr	Ser	Asn	Ser	Pro	Ser	Lys	Glu
		515					520					525			
Ser	Lys	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Ser	Arg	Ile	Leu	Leu	Gly	Lys
	530					535					540				
Thr	Gly	Val	Ile	Lys	Glu	Glu	Pro	Gln	Gln	Asn	Met	Ser	Gln	Pro	Glu
545					550					555					560
Val	Lys	Asp	Pro	Trp	Asn	Leu	Ser	Asn	Asp	Glu	Tyr	Tyr	Tyr	Pro	Lys
			565						570					575	
Gln	Gln	Gly	Leu	Arg	Gly	Thr	Phe	Gly	Gly	Asn	Ile	Ile	Gln	His	Ser
		580						585					590		
Ile	Pro	Ala	Val	Glu	Leu	Arg	Gln	Pro	Phe	Phe	Pro	Thr	His	Met	Gly
		595					600					605			
Pro	Ile	Lys	Leu	Arg	Gln	Phe	His	Arg	Pro	Pro	Leu	Lys	Lys	Tyr	Ser
	610					615					620				
Phe	Gly	Ala	Leu	Ser	Gln	Pro	Gly	Pro	His	Ser	Val	Gln	Pro	Leu	Leu
625					630					635					640
Lys	His	Ile	Lys	Lys	Lys	Ala	Lys	Met	Arg	Glu	Gln	Glu	Arg	Gln	Ala
			645						650					655	
Ser	Gly	Gly	Gly	Glu	Met	Phe	Phe	Met	Arg	Thr	Pro	Gln	Asp	Leu	Thr
		660						665					670		
Gly	Lys	Asp	Gly	Asp	Leu	Ile	Leu	Ala	Glu	Tyr	Ser	Glu	Glu	Asn	Gly
		675					680					685			
Pro	Leu	Met	Met	Gln	Val	Gly	Met	Ala	Thr	Lys	Ile	Lys	Asn	Tyr	Tyr
	690					695					700				
Lys	Arg	Lys	Pro	Gly	Lys	Asp	Pro	Gly	Ala	Pro	Asp	Cys	Lys	Tyr	Gly
705					710					715					720
Glu	Thr	Val	Tyr	Cys	His	Thr	Ser	Pro	Phe	Leu	Gly	Ser	Leu	His	Pro
			725						730					735	
Gly	Gln	Leu	Leu	Gln	Ala	Phe	Glu	Asn	Asn	Leu	Phe	Arg	Ala	Pro	Ile
		740						745					750		
Tyr	Leu	His	Lys	Met	Pro	Glu	Thr	Asp	Phe	Leu	Ile	Ile	Arg	Thr	Arg
		755					760					765			
Gln	Gly	Tyr	Tyr	Ile	Arg	Glu	Leu	Val	Asp	Ile	Phe	Val	Val	Gly	Gln
	770					775					780				
Gln	Cys	Pro	Leu	Phe	Glu	Val	Pro	Gly	Pro	Asn	Ser	Lys	Arg	Ala	Asn
785					790					795					800
Thr	His	Ile	Arg	Asp	Phe	Leu	Gln	Val	Phe	Ile	Tyr	Arg	Leu	Phe	Trp
			805						810					815	
Lys	Ser	Lys	Asp	Arg	Pro	Arg	Arg	Ile	Arg	Met	Glu	Asp	Ile	Lys	Lys
		820						825					830		
Ala	Phe	Pro	Ser	His	Ser	Glu	Ser	Ser	Ile	Arg	Lys	Arg	Leu	Lys	Leu
		835					840					845			
Cys	Ala	Asp	Phe	Lys	Arg	Thr	Gly	Met	Asp	Ser	Asn	Trp	Trp	Val	Leu
	850					855					860				
Lys	Ser	Asp	Phe	Arg	Leu	Pro	Thr	Glu	Glu	Glu	Ile	Arg	Ala	Met	Val
865					870					875					880
Ser	Pro	Glu	Gln	Cys	Cys	Ala	Tyr	Tyr	Ser	Met	Ile	Ala	Ala	Glu	Gln
			885						890					895	
Arg	Leu	Lys	Asp	Ala	Gly	Tyr	Gly	Glu	Lys	Ser	Phe	Phe	Ala	Pro	Glu
		900						905					910		
Glu	Glu	Asn	Glu	Glu	Asp	Phe	Gln	Met	Lys	Ile	Asp	Asp	Glu	Val	Arg
		915					920					925			
Thr	Ala	Pro	Trp	Asn	Thr	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Met	Lys	Gly

930		935		940
Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly				
945		950		955
Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys				960
	965		970	975
Asp Asp Lys Glu Pro Gln Pro Val Lys Thr Val Thr Gly Thr Asp				
	980		985	990
Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg				
	995		1000	1005
Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp Glu				
	1010		1015	1020
Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg Ser Gly				
	1025		1030	1035
Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe Ser Val Ala				1040
	1045		1050	1055
Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg Ile Phe Asp Leu				
	1060		1065	1070
Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu Ser Thr Asp Thr Asp				
	1075		1080	1085
Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu Glu Met Gly Lys Asn Ile				
	1090		1095	1100
Glu Asn Met Leu Gln Asn Lys Lys Thr Ser Ser Gln Leu Ser Arg Glu				
	1105		1110	1115
Arg Glu Glu Gln Glu Arg Lys Glu Leu Gln Arg Met Leu Leu Ala Ala				
	1125		1130	1135
Gly Ser Ala Ala Ser Gly Asn Asn His Arg Asp Asp Asp Thr Ala Ser				
	1140		1145	1150
Val Thr Ser Leu Asn Ser Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr				
	1155		1160	1165
Arg Thr Phe Arg Asp Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr				
	1170		1175	1180
Val Arg Lys Pro Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr				
	1185		1190	1195
Lys Asp Glu Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His				
	1205		1210	1215
Arg Glu Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg				
	1220		1225	1230
Arg Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu				
	1235		1240	1245
Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys Cys				
	1250		1255	1260
Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe Cys Pro				
	1265		1270	1275
Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val Ala Met Thr				
	1285		1290	1295
Glu Glu Gln Glu Glu Leu Glu Lys Thr Val Ile His Asn Asp Asn				
	1300		1305	1310
Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile Val Leu Gly Lys Gln				
	1315		1320	1325
Leu Ile Glu Ser Ala Asp Glu Val Arg Arg Lys Ser Leu Val Leu Lys				
	1330		1335	1340
Phe Pro Lys Gln Gln Leu Pro Pro Lys Lys Lys Arg Arg Val Gly Thr				
	1345		1350	1355
Thr Val His Cys Asp Tyr Leu Asn Arg Pro His Lys Ser Ile His Arg				
	1365		1370	1375
Arg Arg Thr Asp Pro Met Val Thr Leu Ser Ser Ile Leu Glu Ser Ile				
	1380		1385	1390
Ile Asn Asp Met Arg Asp Leu Pro Asn Thr Tyr Pro Phe His Thr Pro				
	1395		1400	1405
Val Asn Ala Lys Val Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro				
	1410		1415	1420

Met	Asp	Leu	Gln	Thr	Leu	Arg	Glu	Asn	Val	Arg	Lys	Arg	Leu	Tyr	Pro	1425	1430	1435	1440
Ser	Arg	Glu	Glu	Phe	Arg	Glu	His	Leu	Glu	Leu	Ile	Val	Lys	Asn	Ser	1445	1450	1455	
Ala	Thr	Tyr	Asn	Gly	Pro	Lys	His	Ser	Leu	Thr	Gln	Ile	Ser	Gln	Ser	1460	1465	1470	
Met	Leu	Asp	Leu	Cys	Asp	Glu	Lys	Leu	Lys	Glu	Lys	Glu	Asp	Lys	Leu	1475	1480	1485	
Ala	Arg	Leu	Glu	Lys	Ala	Ile	Asn	Pro	Leu	Leu	Asp	Asp	Asp	Asp	Gln	1490	1495	1500	
Val	Ala	Phe	Ser	Phe	Ile	Leu	Asp	Asn	Ile	Val	Thr	Gln	Lys	Met	Met	1505	1510	1515	1520
Ala	Val	Pro	Asp	Ser	Trp	Pro	Phe	His	His	Pro	Val	Asn	Lys	Lys	Phe	1525	1530	1535	
Val	Pro	Asp	Tyr	Tyr	Lys	Val	Ile	Val	Asn	Pro	Met	Asp	Leu	Glu	Thr	1540	1545	1550	
Ile	Arg	Lys	Asn	Ile	Ser	Lys	His	Lys	Tyr	Gln	Ser	Arg	Glu	Ser	Phe	1555	1560	1565	
Leu	Asp	Asp	Val	Asn	Leu	Ile	Leu	Ala	Asn	Ser	Val	Lys	Tyr	Asn	Gly	1570	1575	1580	
Pro	Glu	Ser	Gln	Tyr	Thr	Lys	Thr	Ala	Gln	Glu	Ile	Val	Asn	Val	Cys	1585	1590	1595	1600
Tyr	Gln	Thr	Leu	Thr	Glu	Tyr	Asp	Glu	His	Leu	Thr	Gln	Leu	Glu	Lys	1605	1610	1615	
Asp	Ile	Cys	Thr	Ala	Lys	Glu	Ala	Ala	Leu	Glu	Glu	Ala	Glu	Leu	Glu	1620	1625	1630	
Ser	Leu	Asp	Pro	Met	Thr	Pro	Gly	Pro	Tyr	Thr	Pro	Gln	Pro	Pro	Asp	1635	1640	1645	
Leu	Tyr	Asp	Thr	Asn	Thr	Ser	Leu	Ser	Met	Ser	Arg	Asp	Ala	Ser	Val	1650	1655	1660	
Phe	Gln	Asp	Glu	Ser	Asn	Met	Ser	Val	Leu	Asp	Ile	Pro	Ser	Ala	Thr	1665	1670	1675	1680
Pro	Glu	Lys	Gln	Val	Thr	Gln	Glu	Gly	Glu	Asp	Gly	Asp	Gly	Asp	Leu	1685	1690	1695	
Ala	Asp	Glu	Glu	Gly	Thr	Val	Gln	Gln	Pro	Gln	Ala	Ser	Val	Leu		1700	1705	1710	
Tyr	Glu	Asp	Leu	Leu	Met	Ser	Glu	Gly	Glu	Asp	Asp	Glu	Glu	Asp	Ala	1715	1720	1725	
Gly	Ser	Asp	Glu	Glu	Gly	Asp	Asn	Pro	Phe	Ser	Ala	Ile	Gln	Leu	Ser	1730	1735	1740	
Glu	Ser	Gly	Ser	Asp	Ser	Asp	Val	Gly	Ser	Gly	Gly	Ile	Arg	Pro	Lys	1745	1750	1755	1760
Gln	Pro	Arg	Met	Leu	Gln	Glu	Asn	Thr	Arg	Met	Asp	Met	Glu	Asn	Glu	1765	1770	1775	
Glu	Ser	Met	Met	Ser	Tyr	Glu	Gly	Asp	Gly	Gly	Glu	Ala	Ser	His	Gly	1780	1785	1790	
Leu	Glu	Asp	Ser	Asn	Ile	Ser	Tyr	Gly	Ser	Tyr	Glu	Glu	Pro	Asp	Pro	1795	1800	1805	
Lys	Ser	Asn	Thr	Gln	Asp	Thr	Ser	Phe	Ser	Ser	Ile	Gly	Gly	Tyr	Glu	1810	1815	1820	
Val	Ser	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Gln	Arg	Ser	Gly		1825	1830	1835	1840
Pro	Ser	Val	Leu	Ser	Gln	Val	His	Leu	Ser	Glu	Asp	Glu	Glu	Asp	Ser	1845	1850	1855	
Glu	Asp	Phe	His	Ser	Ile	Ala	Gly	Asp	Ser	Asp	Leu	Asp	Ser	Asp	Glu	1860	1865	1870	

<210> 7

<211> 429

<212> PRT

<213> C. albicans

<400> 7

Glu	Leu	Leu	Leu	Asn	Asn	Pro	Leu	Asp	Asn	Ser	Lys	Gln	Asn	Arg	Gln
1				5					10					15	
Lys	Ile	Glu	Asn	Asp	Asn	Thr	Thr	Asn	Asn	Tyr	Asn	Gln	Asn	Asn	Ser
			20					25					30		
Asn	Val	Gln	Asp	Glu	Glu	Glu	Asp	Asp	Asp	Ile	Phe	Asn	Gly	Gln	Ile
		35					40					45			
Asn	Leu	Asp	Lys	Leu	Lys	Leu	Asp	Met	Asn	Asp	Pro	Asn	Leu	Leu	Phe
	50					55					60				
Val	Pro	Ser	Lys	Lys	Val	Asp	Ala	Thr	Lys	Ser	Val	Val	Pro	Ser	Thr
65					70					75					80
Asp	Lys	Leu	Leu	Glu	Leu	Lys	Phe	Asn	Ile	Ser	Asn	Asp	Gln	Glu	Tyr
				85					90					95	
Glu	Leu	Leu	Arg	Lys	Asn	Tyr	Asn	Thr	Lys	Gln	Arg	Ser	Gln	Leu	Ser
			100					105					110		
Asn	Leu	Asn	Ile	Glu	His	Ser	Val	Pro	Ala	Leu	Arg	Leu	Gln	Thr	Pro
		115					120					125			
Tyr	Tyr	Lys	Val	Lys	Leu	Ser	Thr	Asp	Glu	Thr	Arg	Ser	Phe	His	Arg
	130					135					140				
Pro	Val	Phe	Asn	Val	Arg	Pro	Gly	Thr	Leu	Val	Ser	Phe	Ser	Lys	Leu
145					150					155					160
Lys	Leu	Arg	Lys	Arg	Lys	Lys	Asp	Lys	Gly	Lys	Ser	Leu	Gln	Gln	Ile
				165					170					175	
Phe	Ser	Lys	Thr	Ser	Asp	Leu	Thr	Val	Ala	Asp	Thr	Gly	Asn	Ile	Ile
			180					185					190		
Ala	Leu	Glu	Tyr	Ser	Glu	Gln	Tyr	Pro	Pro	Ile	Leu	Ser	Asn	Phe	Gly
		195					200					205			
Met	Gly	Ser	Lys	Leu	Ile	Asn	Tyr	Tyr	Arg	Lys	Glu	Arg	Pro	Asn	Asp
	210					215					220				
Thr	Ser	Arg	Pro	Lys	Ala	Gln	Ile	Gly	Glu	Thr	His	Ile	Leu	Gly	Val
225					230					235					240
Glu	Asp	Arg	Ser	Pro	Phe	Trp	Asn	Phe	Gly	Glu	Val	Ala	Pro	Gly	Asp
				245					250					255	
Phe	Val	Pro	Thr	Leu	Tyr	Asn	Asn	Met	Val	Arg	Ala	Pro	Ile	Phe	Lys
			260					265					270		
His	Asp	Asn	Lys	Pro	Thr	Asp	Phe	Leu	Leu	Val	Lys	Ser	Gln	Gly	Ala
		275					280					285			
Gly	Ser	His	Gln	Lys	Phe	Tyr	Leu	Arg	Gly	Ile	Asn	Phe	Asn	Phe	Ala
	290					295					300				
Val	Gly	Asn	Thr	Phe	Pro	Val	Glu	Val	Pro	Ala	Pro	His	Ser	Arg	Lys
305					310					315					320
Val	Thr	Asn	Ile	Ser	Lys	Asn	Arg	Leu	Lys	Met	Val	Val	Phe	Arg	Val
				325					330					335	
Met	Asn	Ser	Leu	Gly	Val	Pro	Arg	Ile	Ser	Val	Lys	Asp	Val	Ser	Lys
			340					345					350		
His	Phe	Pro	Glu	His	Ser	Asp	Met	Gln	Asn	Arg	Gln	Arg	Leu	Lys	Glu
		355					360					365			
Phe	Met	Glu	Tyr	Gln	Arg	Gln	Gly	Glu	Asp	Gln	Gly	Tyr	Trp	Lys	Val
	370					375					380				
Arg	Gly	Leu	Asn	Asp	Val	Ile	Pro	Gly	Glu	Glu	Glu	Ile	Arg	Thr	Met
385					390					395					400
Ile	Thr	Pro	Glu	Asp	Ser	Ser	Leu	Met	Asp	Thr	Met	Gln	Phe	Gly	Gln
				405					410					415	
Gln	Val	Leu	Asp	Asp	Asn	Met	Val	Leu	Phe	Gly	Glu	Gln			
			420					425							

<210> 8
 <211> 434
 <212> PRT
 <213> S. cerevisiae

<400> 8

Met	Thr	Pro	Asn	Leu	Lys	Phe	Ser	Gly	Gly	Tyr	Lys	Leu	Lys	Ser	Leu
1				5					10					15	
Ile	Glu	Asp	Val	Ala	Glu	Asp	Trp	Gln	Trp	Asp	Glu	Asp	Met	Ile	Ile
			20					25					30		
Asp	Ala	Lys	Leu	Lys	Glu	Ser	Lys	His	Ala	Glu	Leu	Asn	Met	Asn	Asp
		35					40					45			
Glu	Lys	Leu	Leu	Leu	Met	Ile	Glu	Lys	Thr	Asn	Asn	Leu	Ala	Gln	Gln
	50					55					60				
Lys	Gln	Gln	Leu	Asp	Ser	Ser	Asn	Leu	Ile	Leu	Pro	Leu	Asn	Glu	Thr
65					70					75					80
Ile	Leu	Gln	Gln	Lys	Phe	Asn	Leu	Ser	Asn	Asp	Asp	Lys	Tyr	Gln	Ile
				85					90					95	
Leu	Lys	Lys	Thr	His	Gln	Thr	Lys	Val	Arg	Ser	Thr	Ile	Ser	Asn	Leu
			100					105					110		
Asn	Ile	Gln	His	Ser	Gln	Pro	Ala	Ile	Asn	Leu	Gln	Ser	Pro	Phe	Tyr
		115					120					125			
Lys	Val	Ala	Val	Pro	Arg	Tyr	Gln	Leu	Arg	His	Phe	His	Arg	Glu	Asn
	130						135				140				
Phe	Gly	Ser	His	Ile	Arg	Pro	Gly	Thr	Lys	Ile	Val	Phe	Ser	Lys	Leu
145					150					155					160
Lys	Ala	Arg	Lys	Arg	Lys	Arg	Asp	Lys	Gly	Lys	Asp	Val	Lys	Glu	Ser
				165					170					175	
Phe	Ser	Thr	Ser	Gln	Asp	Leu	Thr	Ile	Gly	Asp	Thr	Ala	Pro	Val	Tyr
			180					185					190		
Leu	Met	Glu	Tyr	Ser	Glu	Gln	Thr	Pro	Val	Ala	Leu	Ser	Lys	Phe	Gly
	195						200					205			
Met	Ala	Asn	Lys	Leu	Ile	Asn	Tyr	Tyr	Arg	Lys	Ala	Asn	Glu	Gln	Asp
	210					215					220				
Thr	Leu	Arg	Pro	Lys	Leu	Pro	Val	Gly	Glu	Thr	His	Val	Leu	Gly	Val
225					230					235					240
Gln	Asp	Lys	Ser	Pro	Phe	Trp	Asn	Phe	Gly	Phe	Val	Glu	Pro	Gly	His
				245					250					255	
Ile	Val	Pro	Thr	Leu	Tyr	Asn	Asn	Met	Ile	Arg	Ala	Pro	Val	Phe	Lys
			260					265					270		
His	Asp	Ile	Ser	Gly	Thr	Asp	Phe	Leu	Leu	Thr	Lys	Ser	Ser	Gly	Phe
	275						280					285			
Gly	Ile	Ser	Asn	Arg	Phe	Tyr	Leu	Arg	Asn	Ile	Asn	His	Leu	Phe	Thr
	290					295				300					
Val	Gly	Gln	Thr	Phe	Pro	Val	Glu	Glu	Ile	Pro	Gly	Pro	Asn	Ser	Arg
305					310					315					320
Lys	Val	Thr	Ser	Met	Lys	Ala	Thr	Arg	Leu	Lys	Met	Ile	Ile	Tyr	Arg
				325					330					335	
Ile	Leu	Asn	His	Asn	His	Ser	Lys	Ala	Ile	Ser	Ile	Asp	Pro	Ile	Ala
			340					345					350		
Lys	His	Phe	Pro	Asp	Gln	Asp	Tyr	Gly	Gln	Asn	Arg	Gln	Lys	Val	Lys
		355					360					365			
Glu	Phe	Met	Lys	Tyr	Gln	Arg	Asp	Gly	Pro	Glu	Lys	Gly	Leu	Trp	Arg
	370					375					380				
Leu	Lys	Asp	Asp	Glu	Lys	Leu	Leu	Asp	Asn	Glu	Ala	Val	Lys	Ser	Leu
385					390					395					400
Ile	Thr	Pro	Glu	Gln	Ile	Ser	Gln	Val	Glu	Ser	Met	Ser	Gln	Gly	Leu
				405					410					415	
Gln	Phe	Gln	Glu	Asp	Asn	Glu	Ala	Tyr	Asn	Phe	Asp	Ser	Lys	Leu	Lys
			420					425					430		

Ser Leu

<210> 9
<211> 415

<212> PRT

<213> S. pombe

<400> 9

Val	Asn	Lys	Thr	Asn	Gln	Ser	Ser	Phe	Phe	Ile	Asp	Lys	Ser	Leu	Val
1				5					10					15	
Asp	Ile	Asp	Phe	Ala	Phe	Asp	Glu	Asn	Ile	Phe	Asp	Gly	Asp	Thr	Gly
			20					25					30		
Thr	Ser	Lys	Val	Val	Leu	Asn	Leu	Asn	Asp	Pro	Lys	Leu	Leu	Leu	Gln
		35					40					45			
Pro	Gln	Leu	Pro	Lys	Lys	Glu	Asp	Ser	Gln	Arg	Ser	Phe	Ala	Asp	Thr
	50					55					60				
His	Gln	Arg	Asn	Ser	Leu	Ala	Trp	Lys	Phe	Asn	Ile	Ser	Asn	Asp	Pro
65					70					75				80	
Ala	Tyr	Glu	Met	Leu	Lys	Gln	Asn	His	Gln	Ser	Lys	Val	Arg	Asn	Thr
			85					90						95	
Leu	Ser	Gln	Leu	Ala	Ile	Glu	His	Ala	Ala	Phe	Ala	Glu	Lys	Leu	Thr
		100						105					110		
Phe	Pro	Tyr	Tyr	Lys	Thr	Arg	Leu	Ser	Lys	Arg	Ala	Val	Arg	Ser	Tyr
	115						120					125			
His	Arg	Pro	Thr	Met	Ser	Phe	Lys	Pro	Asn	Ala	Ala	Ile	Val	Phe	Ser
	130					135					140				
Pro	Leu	Ile	Val	Arg	Lys	Arg	Ser	Lys	Asp	Lys	His	Lys	Ser	Glu	Arg
145					150				155					160	
Glu	Leu	Ile	Pro	Thr	Thr	Lys	Glu	Ile	Thr	Met	Gly	Asp	Thr	Thr	His
			165					170						175	
Ala	Ile	Leu	Val	Glu	Phe	Ser	Glu	Glu	His	Pro	Ala	Val	Leu	Ser	Asn
		180						185					190		
Ala	Gly	Met	Ala	Ser	Arg	Ile	Val	Asn	Tyr	Tyr	Arg	Lys	Lys	Asn	Glu
	195						200					205			
Gln	Asp	Glu	Ser	Arg	Pro	Lys	Leu	Glu	Val	Gly	Glu	Ser	His	Val	Leu
	210					215					220				
Asp	Val	Gln	Asp	Arg	Ser	Pro	Phe	Trp	Asn	Phe	Gly	Ser	Val	Glu	Pro
225					230					235				240	
Gly	Glu	Ile	Thr	Pro	Thr	Leu	Tyr	Asn	Lys	Met	Ile	Arg	Ala	Pro	Leu
			245						250					255	
Phe	Lys	His	Glu	Val	Pro	Pro	Thr	Asp	Phe	Ile	Leu	Ile	Arg	Asn	Ser
		260						265					270		
Ser	Ser	Tyr	Gly	Ser	Lys	Tyr	Tyr	Leu	Lys	Asn	Ile	Asn	His	Met	Phe
	275						280					285			
Val	Ser	Gly	Gln	Thr	Phe	Pro	Val	Thr	Asp	Val	Pro	Gly	Pro	His	Ser
	290					295					300				
Arg	Lys	Val	Thr	Thr	Ala	Ser	Lys	Asn	Arg	Leu	Lys	Met	Leu	Val	Phe
305					310					315				320	
Arg	Leu	Ile	Arg	Arg	Ser	Pro	Asn	Gly	Gly	Leu	Phe	Ile	Arg	Gln	Leu
			325						330					335	
Ser	Lys	His	Phe	Ser	Asp	Gln	Asn	Glu	Met	Gln	Ile	Arg	Gln	Arg	Leu
		340						345					350		
Lys	Glu	Phe	Met	Glu	Tyr	Lys	Lys	Lys	Gly	Asp	Gly	Pro	Gly	Tyr	Trp
	355					360					365				
Lys	Leu	Lys	Ser	Asn	Glu	Val	Val	Pro	Asp	Glu	Ala	Gly	Thr	Arg	Ser
	370					375					380				
Met	Val	Ser	Pro	Glu	Thr	Val	Cys	Leu	Leu	Glu	Ser	Met	Gln	Val	Gly
385				390						395					400
Val	Arg	Gln	Leu	Glu	Asp	Ala	Gly	Tyr	Gly	Lys	Thr	Met	Asp	Glu	
			405						410					415	

<210> 10

<211> 481

<212> PRT

<213> Homo sapiens

<400> 10

Ser	Leu	Ala	Gly	Trp	Leu	Pro	Ser	Ser	Met	Thr	Arg	Asn	Ala	Met	Ala
1			5						10					15	
Tyr	Asn	Val	Gln	Gly	Phe	Ala	Ala	Ala	Thr	Leu	Asp	Asp	Asp	Lys	Pro
			20					25					30		
Trp	Tyr	Ser	Ile	Phe	Pro	Ile	Asp	Asn	Glu	Asp	Leu	Val	Tyr	Gly	Arg
		35					40					45			
Trp	Glu	Asp	Asn	Ile	Ile	Trp	Asp	Ala	Gln	Ala	Met	Pro	Arg	Leu	Leu
	50						55				60				
Glu	Pro	Pro	Val	Leu	Thr	Leu	Asp	Pro	Asn	Asp	Glu	Asn	Leu	Ile	Leu
65					70					75					80
Glu	Ile	Pro	Asp	Glu	Lys	Glu	Glu	Ala	Thr	Ser	Asn	Ser	Pro	Ser	Lys
					85				90					95	
Glu	Ser	Lys	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Ser	Arg	Ile	Leu	Leu	Gly
			100					105					110		
Lys	Thr	Gly	Val	Ile	Lys	Glu	Glu	Pro	Gln	Gln	Asn	Met	Ser	Gln	Pro
		115						120				125			
Glu	Val	Lys	Asp	Pro	Trp	Asn	Leu	Ser	Asn	Asp	Glu	Tyr	Tyr	Tyr	Pro
	130					135					140				
Lys	Gln	Gln	Gly	Leu	Arg	Gly	Thr	Phe	Gly	Gly	Asn	Ile	Ile	Gln	His
145					150					155					160
Ser	Ile	Pro	Ala	Val	Glu	Leu	Arg	Gln	Pro	Phe	Phe	Pro	Thr	His	Met
				165					170					175	
Gly	Pro	Ile	Lys	Leu	Arg	Gln	Phe	His	Arg	Pro	Pro	Leu	Lys	Lys	Tyr
			180					185					190		
Ser	Phe	Gly	Ala	Leu	Ser	Gln	Pro	Gly	Pro	His	Ser	Val	Gln	Pro	Leu
	195						200					205			
Leu	Lys	His	Ile	Lys	Lys	Lys	Ala	Lys	Met	Arg	Glu	Gln	Glu	Arg	Gln
	210					215					220				
Ala	Ser	Gly	Gly	Gly	Glu	Met	Phe	Phe	Met	Arg	Thr	Pro	Gln	Asp	Leu
225					230					235					240
Thr	Gly	Lys	Asp	Gly	Asp	Leu	Ile	Leu	Ala	Glu	Tyr	Ser	Glu	Glu	Asn
				245					250					255	
Gly	Pro	Leu	Met	Met	Gln	Val	Gly	Met	Ala	Thr	Lys	Ile	Lys	Asn	Tyr
			260					265					270		
Tyr	Lys	Arg	Lys	Pro	Gly	Lys	Asp	Pro	Gly	Ala	Pro	Asp	Cys	Lys	Tyr
	275						280					285			
Gly	Glu	Thr	Val	Tyr	Cys	His	Thr	Ser	Pro	Phe	Leu	Gly	Ser	Leu	His
	290					295					300				
Pro	Gly	Gln	Leu	Leu	Gln	Ala	Phe	Glu	Asn	Asn	Leu	Phe	Arg	Ala	Pro
305					310					315					320
Ile	Tyr	Leu	His	Lys	Met	Pro	Glu	Thr	Asp	Phe	Leu	Ile	Ile	Arg	Thr
				325					330					335	
Arg	Gln	Gly	Tyr	Tyr	Ile	Arg	Glu	Leu	Val	Asp	Ile	Phe	Val	Val	Gly
			340					345					350		
Gln	Gln	Cys	Pro	Leu	Phe	Glu	Val	Pro	Gly	Pro	Asn	Ser	Lys	Arg	Ala
		355					360					365			
Asn	Thr	His	Ile	Arg	Asp	Phe	Leu	Gln	Val	Phe	Ile	Tyr	Arg	Leu	Phe
	370					375					380				
Trp	Lys	Ser	Lys	Asp	Arg	Pro	Arg	Arg	Ile	Arg	Met	Glu	Asp	Ile	Lys
385					390					395					400
Lys	Ala	Phe	Pro	Ser	His	Ser	Glu	Ser	Ser	Ile	Arg	Lys	Arg	Leu	Lys
				405					410					415	
Leu	Cys	Ala	Asp	Phe	Lys	Arg	Thr	Gly	Met	Asp	Ser	Asn	Trp	Trp	Val
		420						425					430		
Leu	Lys	Ser	Asp	Phe	Arg	Leu	Pro	Thr	Glu	Glu	Glu	Ile	Arg	Ala	Met
	435						440					445			
Val	Ser	Pro	Glu	Gln	Cys	Cys	Ala	Tyr	Tyr	Ser	Met	Ile	Ala	Ala	Glu
	450					455					460				
Gln	Arg	Leu	Lys	Asp	Ala	Gly	Tyr	Gly	Glu	Lys	Ser	Phe	Phe	Ala	Pro

465
Glu

470

475

480

<210> 11
<211> 74
<212> PRT
<213> C. albicans

<400> 11
Asp Ala Glu Asn Gly Asp Asp Ile Asn Lys Asp Lys Glu Lys Glu Val
1 5 10 15
Glu Lys Glu Lys Glu Gln Glu Arg Glu Glu Lys Gly Lys Asp Lys
20 25 30
Glu Lys Asp Lys Asp Lys Glu Lys Asp Lys Thr Glu Lys Glu Lys Ser
35 40 45
Lys Lys Ser Lys Glu Gln Asp Thr Glu Ile Asp Val Glu Glu Glu Leu
50 55 60
Ala Pro Trp Asn Leu Ser Arg Asn Phe Val
65 70

<210> 12
<211> 18
<212> DNA
<213> "Artificial Sequence"
<220>

<223> sequence source: Degenerate oligonucleotide designed and
used to amplify fragments of DNA from Candida albicans strain
SC5314 genomic DNA by polymerase chain reaction. n is defined as
Inosine.

<400> 12
ccwggwccwa aytcnadd 18

<210> 13
<211> 23
<212> DNA
<213> "Artificial Sequence"
<220>

<223> sequence source: Degenerate oligonucleotide designed and
used to amplify fragments of DNA from Candida albicans strain
SC5314 genomic DNA by polymerase chain reaction.

<400> 13
gayccwachg gwtgtggwga agg 23

<210> 14
<211> 24
<212> DNA
<213> "Artificial Sequence"
<220>

<223> sequence source: Degenerate oligonucleotide designed and
used to amplify fragments of DNA from Candida albicans strain
SC5314 genomic DNA by polymerase chain reaction.

<400> 14
cctttcwcca cawccagtwg grtc 24

<210> 15
<211> 19
<212> DNA

<213> "Artificial Sequence"
 <220>
 <223> sequence source: Degenerate oligonucleotide designed and
 used to amplify fragments of DNA from Candida albicans strain
 SC5314 genomic DNA by polymerase chain reaction. n is defined as
 Inosine.

<400> 15
 ttrttthcayc tnartgwcc 19

<210> 16
 <211> 30
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> S. cerevisiae

<400> 16
 ccgctcgaga tgacacccaa cttaaagttc 30

<210> 17
 <211> 29
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> S. cerevisiae

<400> 17
 cgcggatcca gagattttag cttagaatc 29

<210> 18
 <211> 37
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> C. albicans

<400> 18
 ggaattccat atgcttttgc tcaacaatcc cttggac 37

<210> 19
 <211> 32
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> C. albicans

<400> 19
 cgcggatecc tgctctgctc accgaataac ac 32

<210> 20
 <211> 37
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> Homo sapiens

<400> 20
 ggaattccat atgagcctgg caggctggct tccttct 37

<210> 21
 <211> 33
 <212> DNA

<213> "Artificial Sequence"
 <220>
 <223> Homo sapiens
 <400> 21
 ccgctcgagt tctggagcaa aaaaggattt ctc

33

<210> 22
 <211> 0
 <212> DNA
 <213> Homo sapiens
 <400> 22
 Met Gly Pro Gly Cys Asp Leu Leu Leu Arg Thr Ala Ala Thr Ile Thr
 1 5 10 15
 Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
 20 25 30
 Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
 35 40 45
 Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
 50 55 60
 His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
 65 70 75 80
 Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
 85 90 95
 Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
 100 105 110
 Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
 115 120 125
 Gly Ser Leu Gln Pro Leu Cys His Ser Asp Tyr Asp Glu Asp Asp Tyr
 130 135 140
 Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
 145 150 155 160
 Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
 165 170 175
 Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met
 180 185 190
 Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
 195 200 205
 Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
 210 215 220
 Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
 225 230 235 240
 Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
 245 250 255
 Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
 260 265 270
 Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
 275 280 285
 Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
 290 295 300
 Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
 305 310 315 320
 Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
 325 330 335
 Arg Val Ala Glu Trp Arg Tyr Gly Pro Ala Arg Leu Trp Tyr Asp Met
 340 345 350
 Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
 355 360 365
 Arg Lys Thr Glu His Glu Pro Val Ile Lys Ser Arg Met Ile Glu Glu
 370 375 380
 Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu

385	Asn	Phe	Leu	Met	Val	Thr	Gln	Leu	His	Trp	Glu	Asp	Asp	Ile	Ile	Trp
				405						410					415	
	Asp	Gly	Glu	Asp	Val	Lys	His	Lys	Gly	Thr	Lys	Pro	Gln	Arg	Ala	Ser
				420					425						430	
	Leu	Ala	Gly	Trp	Leu	Pro	Ser	Ser	Met	Thr	Arg	Asn	Ala	Met	Ala	Tyr
			435					440					445			
	Asn	Val	Gln	Gln	Gly	Phe	Ala	Ala	Thr	Leu	Asp	Asp	Asp	Lys	Pro	Trp
		450				455					460					
	Tyr	Ser	Ile	Phe	Pro	Ile	Asp	Asn	Glu	Asp	Leu	Val	Tyr	Gly	Arg	Trp
465						470				475						480
	Glu	Asp	Asn	Ile	Ile	Trp	Asp	Ala	Gln	Ala	Met	Pro	Arg	Leu	Leu	Glu
				485					490						495	
	Pro	Pro	Val	Leu	Thr	Leu	Asp	Pro	Asn	Asp	Glu	Asn	Leu	Ile	Leu	Glu
			500						505					510		
	Ile	Pro	Asp	Glu	Lys	Glu	Glu	Ala	Thr	Ser	Asn	Ser	Pro	Ser	Lys	Glu
		515						520					525			
	Ser	Lys	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Ser	Arg	Ile	Leu	Leu	Gly	Lys
		530					535					540				
	Thr	Gly	Val	Ile	Lys	Glu	Glu	Pro	Gln	Gln	Asn	Met	Ser	Gln	Pro	Glu
545						550					555					560
	Val	Lys	Asp	Pro	Trp	Asn	Leu	Ser	Asn	Asp	Glu	Tyr	Tyr	Tyr	Pro	Lys
				565					570						575	
	Gln	Gln	Gly	Leu	Arg	Gly	Thr	Phe	Gly	Gly	Asn	Ile	Ile	Gln	His	Ser
			580					585						590		
	Ile	Pro	Ala	Val	Glu	Leu	Arg	Gln	Pro	Phe	Phe	Pro	Thr	His	Met	Gly
		595					600						605			
	Pro	Ile	Lys	Leu	Arg	Gln	Phe	His	Arg	Pro	Pro	Leu	Lys	Lys	Tyr	Ser
		610				615						620				
	Phe	Gly	Ala	Leu	Ser	Gln	Pro	Gly	Pro	His	Ser	Val	Gln	Pro	Leu	Leu
625						630					635					640
	Lys	His	Ile	Lys	Lys	Lys	Ala	Lys	Met	Arg	Glu	Gln	Glu	Arg	Gln	Ala
				645					650						655	
	Ser	Gly	Gly	Gly	Glu	Met	Phe	Phe	Met	Arg	Thr	Pro	Gln	Asp	Leu	Thr
			660					665						670		
	Gly	Lys	Asp	Gly	Asp	Leu	Ile	Leu	Ala	Glu	Tyr	Ser	Glu	Glu	Asn	Gly
		675					680						685			
	Pro	Leu	Met	Met	Gln	Val	Gly	Met	Ala	Thr	Lys	Ile	Lys	Asn	Tyr	Tyr
		690				695					700					
	Lys	Arg	Lys	Pro	Gly	Lys	Asp	Pro	Gly	Ala	Pro	Asp	Cys	Lys	Tyr	Gly
705					710					715						720
	Glu	Thr	Val	Tyr	Cys	His	Thr	Ser	Pro	Phe	Leu	Gly	Ser	Leu	His	Pro
				725					730						735	
	Gly	Gln	Leu	Leu	Gln	Ala	Phe	Glu	Asn	Asn	Leu	Phe	Arg	Ala	Pro	Ile
			740					745					750			
	Tyr	Leu	His	Lys	Met	Pro	Glu	Thr	Asp	Phe	Leu	Ile	Ile	Arg	Thr	Arg
		755					760					765				
	Gln	Gly	Tyr	Tyr	Ile	Arg	Glu	Leu	Val	Asp	Ile	Phe	Val	Val	Gly	Gln
		770				775					780					
	Gln	Cys	Pro	Leu	Phe	Glu	Val	Pro	Gly	Pro	Asn	Ser	Lys	Arg	Ala	Asn
785					790					795						800
	Thr	His	Ile	Arg	Asp	Phe	Leu	Gln	Val	Phe	Ile	Tyr	Arg	Leu	Phe	Trp
				805					810						815	
	Lys	Ser	Lys	Asp	Arg	Pro	Arg	Arg	Ile	Arg	Met	Glu	Asp	Ile	Lys	Lys
			820					825						830		
	Ala	Phe	Pro	Ser	His	Ser	Glu	Ser	Ser	Ile	Arg	Lys	Arg	Leu	Lys	Leu
		835					840						845			
	Cys	Ala	Asp	Phe	Lys	Arg	Thr	Gly	Met	Asp	Ser	Asn	Trp	Trp	Val	Leu
		850				855					860					
	Lys	Ser	Asp	Phe	Arg	Leu	Pro	Thr	Glu	Glu	Glu	Ile	Arg	Ala	Met	Val
865					870					875						880

Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln
 885 890 895
 Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu
 900 905 910
 Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
 915 920 925
 Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly
 930 935 940
 Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
 945 950 955 960
 Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
 965 970 975
 Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp
 980 985 990
 Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg
 995 1000 1005
 Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp Glu
 1010 1015 1020
 Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg Ser Gly
 1025 1030 1035 1040
 Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe Ser Val Ala
 1045 1050 1055
 Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg Ile Phe Asp Leu
 1060 1065 1070
 Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu Ser Thr Asp Thr Asp
 1075 1080 1085
 Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu Glu Met Gly Lys Asn Ile
 1090 1095 1100
 Glu Asn Met Leu Gln Asn Lys Lys Thr Ser Ser Gln Leu Ser Arg Glu
 1105 1110 1115 1120
 Arg Glu Glu Gln Glu Arg Lys Glu Leu Gln Arg Met Leu Leu Ala Ala
 1125 1130 1135
 Gly Ser Ala Ala Ser Gly Asn Asn His Arg Asp Asp Asp Thr Ala Ser
 1140 1145 1150
 Val Thr Ser Leu Asn Ser Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr
 1155 1160 1165
 Arg Thr Phe Arg Asp Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr
 1170 1175 1180
 Val Arg Lys Pro Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr
 1185 1190 1195 1200
 Lys Asp Glu Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His
 1205 1210 1215
 Arg Glu Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg
 1220 1225 1230
 Arg Leu

<210> 23
 <211> 52
 <212> DNA
 <213> C. albicans

<400> 23
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52

<210> 24
 <211> 38
 <212> DNA
 <213> C. albicans

<400> 24
 atagttagcg gccgcacact gctggtgtca accaacia

38

<210> 25
 <211> 52
 <212> DNA
 <213> Homo sapiens

 <400> 25
 acgcgtcgac atgcatcatc atcatcatca tatgggaccc ggctgcgatt tg 52

 <210> 26
 <211> 31
 <212> DNA
 <213> Homo sapiens

 <400> 26
 gttgctctgc agctatcatg ctataataag c 31

 <210> 27
 <211> 31
 <212> DNA
 <213> Homo sapiens

 <400> 27
 tgatagctgc agagcaacga ctgaaggatg c 31

 <210> 28
 <211> 32
 <212> DNA
 <213> Homo sapiens

 <400> 28
 ccggtacctt cccgatgttg ttcatcaaaa ag 32

 <210> 29
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 <212> DNA
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 <223> C. albicans

 <400> 29
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 <210> 30
 <211> 42
 <212> DNA
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 <210> 31
 <211> 41
 <212> DNA
 <213> "Artificial Sequence"
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 <223> C. albicans

 <400> 31

aaaactgcag cgcggatccg cgtgcaggtg acgttattgg a

41

<210> 32

<211> 36

<212> DNA

<213> "Artificial Sequence"

<220>

<223> C. albicans

<400> 32

atagtttagc ggccgccttg tgacaagaag tgacac

36

C1
conclude